

M., Rose, M., Rose, R., Stokes, P., Timney, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10Kb
plasmid inserts

REFERENCE AUTHORS

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddun-genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0011 row: K column: 21
Seq primer: CTTGTGTAACACACGCCGACG
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers

FEATURES source

1..19
/organism="Mus musculus"
/strain="C57H1/6J"
/db_xref="taxon:10090"
/clone_lib="MGI11E21"
/clone_lib="Mouse 10kb plasmid MGI11E21 library"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: pMW22ny; Purified genomic DNA from M.
musculus (C57H1/6J) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMW22 (g:14732114:gbAF129072.1), a copy number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT 4 a 5 c 3 g 7 t

ORIGIN

Alignment Scores:
Prod. No.: 1,26c+03 Length: 19
Score: 23.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 17 Gaps: 0

US-09-856-070-25 (1-5) x AW423440 (1-19)

QY 1 MetLeuAraLeuGln 5

DB 16 ATGCTAGATTACAG 2

RESULT 2

AW423440/c
Locus SB66102 (1-5) x AW423440 (1-19)
DEFINITION Gm-c1015-4780 5' mRNA sequence.
ACCESSION AW423440
VERSION AW423440.1 GI:6951372
KEYWORDS EST
SOURCE soybean.
ORGANISM Glycine max

Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicot,
Rosidae, eurosids 1, Fabales, Fabaceae, Papilionoideae, Phaseolaceae,
Glycine.

REFERENCE AUTHORS

1 (bases 1 to 54)
Shoemaker, P., Keim, P., Vodkin, L., Erpelidg, J., Coryell, V., Khanna
A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C.,
Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers
J., Person, B., Swaiter, J., Gibbons, M., Fape, D., Harvey, N., Schurk
R., Ritter, E., Kohn, S., Shih, J., Jackson, Y., Caidenas, M., McCann
R., Waterston, R. and Willson, R.
Public Soybean EST Project
Unpublished (1999)

TITLE JOURNAL COMMENT

Contact: Shoemaker P/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu

This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntville, AL 35801 For further information
call: (800)-533-4363 or contact via email: cgen@resgen.com
Insert Length: 271 Std Error: 0.00
Seq primer: -40pp from Gibco.

FEATURES Source

1..54
/organism="Glycine max"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1015-4780"
/clone_lib="Gm-c1015"
/tissue_type="Mature flowers, field grown plants"
/lab_host="XL10-Gold"
/note="Vector: pBluescript II XR; Site_1: EcoRI; Site_2:
XhoI; this cDNA library was constructed from mRNA isolated
from mature flowers of field grown plants. The cDNA
library was prepared using the Stratagene pBluescript II
XR cDNA library construction kit. Complementary DNA was
synthesized from mRNA using a primer consisting of a poly
(dT) sequence with a XhoI restriction site. EcoRI adaptors
were ligated to the blunt-ended cDNA fragments followed by
XhoI digestion. The cDNA fragments were directionally
cloned into the EcoRI-XhoI restriction site of the
pBluescript vector. The ligated cDNA fragments were
transformed into XL10 Gold host cells. This library was
constructed by Dr. Randy Shoemaker and Dr. John
Erpelidg."

BASE COUNT 11 a 7 c 16 q 20 t

ORIGIN

Alignment Scores:
Prod. No.: 4.17e+03 Length: 54
Score: 23.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-09-856-070-25 (1-5) x AW423440 (1-54)

QY 1 MetLeuAraLeuGln 5

DB 27 ATGCTTAGACTTCAA 13

RESULT 3

BF456263
Locus UI-M-B21-Bkv-a-11-0-UI-s1 NIH-BMAP_MHI2.S1
DEFINITION UI-M-B21-Bkv-a-11-0-UI-s1 Mus musculus cDNA clone
BF456263
ACCESSION BF456263
VERSION BF456263.1 GI:11522432
KEYWORDS EST
SOURCE house mouse.

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 66)
AUTHORS Honaldo M.P., Lennon, G., and Soares, M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 9704477
COMMENT Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd Room 7N-7190, MSC 9643 Bethesda, MD
20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
Email: mst@mail.nih.gov
The sequence contained an oligo dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to verify it as a clone from the hippocampus tissue cDNA Library Preparation. M.B. Soares from the distribution: Researchers may obtain BMAP cDNA clones from REFSEARCH GENETICS. It should be noted that Bento Soares is generating a small number of additional specialized non redundant arrays of BMAP cDNAs whose availability will be considered under appropriate and limited collaborative arrangements
Seq primer: M13 Forward
POLVA-Yes.

FEATURES
Source Location/Qualifiers

1..66
/organism="Mus musculus"
/strain="C57Bl/6J"
/db_xref="taxon:10090"
/clone="U1 M-B1-bkv-a-11-G-U1"
/clone_lib="NIH-BMAP_MHI2_S1"
/seq_start="27-32 days"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT73b-Pac (Pharmacia) with a modified polylinker. Site 1 NotI, Site 2 EcoRI, The NIH-BMAP_MHI2_S1 library is a subtracted library derived from NIH-BMAP_MHI2. NIH-BMAP_MHI2 is a library derived from mouse hippocampus tissue. For a detailed description of the library from which this clone was derived, please visit our web site at brainest.org.iowa.edu.
TAG_LIB="NIH-BMAP_MHI2_S1"
TAG_SEQ="TAGTC"

BASE COUNT 19 a 16 c 16 q 15 t

ORIGIN
Alignment Scores:
Pred. No.: 5,25e+03 Length: 66
Score: 23.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-09-856-070-25 (1-5) x H455244 (1-66)

Qy 1 MetLeuArgLeuGln 5
|||||

Db 36 ATGCTGGCGGTTCAA 50

RESULT 4

AZ417551

LOCUS

DEFINITION 1M0193113F Mouse 10kb Plasmid U09C1M library Mus musculus genomic clone U09C1M0193113 F. DNA sequence.

ACCESSION AZ417551

VERSION AZ417551.1 GI:10541564

KEYWORDS GSS

SOURCE
ORGANISM

REFERENCE
AUTHORS

TITLE
JOURNAL

COMMENT

house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 66)
Poulsen, A., Yari, A., Barber, M., Reardon, T., Durai, B., Hamill, C.,
Islam, H., Londeux, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
M., Pose, M., Pose, P., Stokes, P., Tinney, A., von Niederhausern, A.
and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Pm 308, Biomedical Building Research Bldg., 20 E. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5706
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: G193 Row: 1 Column: 13
Seq primer: CGTGTGTAAGGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 66.
Location/Qualifiers
1..66
/organism="Mus musculus"
/strain="C57Bl/6J"
/db_xref="taxon:10090"
/clone="U09C1M0193113"
/clone_lib="Mouse 10kb plasmid U09C1M library"
/sex="Male"

BASE COUNT 14 a 20 c 17 q 15 t

ORIGIN
Alignment Scores:
Pred. No.: 5,25e+03 Length: 66
Score: 23.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 17 Gaps: 0

US-09-856-070-25 (1-5) x AZ417551 (1-66)

Qy 1 MetLeuArgLeuGln 5
|||||

Db 24 ATGCTGGCGGTTCAG 38

RESULT 5

AA016604/c

LOCUS

AA016604

70 bp mpna 1;near EST 02-AUG-1996

```

mq91e07.r1 Soares mouse embryo NMEL13.5.14.5 Mus musculus cDNA
clone IMAGE:440388 5' similar to PIR:A42792 A42792 succinate
dehydrogenase ;, mRNA sequence.
ACCESSION      AA016604
VERSION        AA016604.1  GI:1478965
KEYWORDS       EST.
SOURCE         house mouse
ORGANISM       Mus musculus
REFERENCE      Mammalia: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
AUTHORS        Murra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
                Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
                Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
                Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                Waterston, R.
TITLE          The WashU-HMI Mouse EST Project
JOURNAL        Unpublished (1996)
COMMENT        Contact: Marra M/Mouse EST Project
                WashU-HMI Mouse EST Project
                Washington University School of Medicine
                4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                Tel: 314 286 1800
                Fax: 314 286 1810
                Email: mouseest@watson.wustl.edu
                This clone is available royalty-free through LLNL ; contact the
                IMAGE Consortium (info@imgc.llnl.gov) for further information.
                MGI:265724
                Trace considered overall poor quality
                Possible reversed clone, similarity on wrong strand
                Seq primer: -28M13 rev2 from Amersham
                High quality sequence stop: 1.
FEATURES       1..70
                Location/Qualifiers
                1..70
                /organism="Mus musculus"
                /strain="C57BL/6J"
                /db_xref="taxon:10090"
                /clone="IMAGE:440388"
                /clone_lib="Soares mouse embryo NMEL13.5.14.5"
                /sex="unknown"
                /tissue_type="embryo"
                /dev_stage="13.5-14.5dpc total telus"
                /lab_host="DH10B"
                /note="Vector: p773D-Pac (Pharmacia) with a modified
                polylinker; Site 1: Not 1; Site 2: Eco RI; 1st strand cDNA
                was primed with a Not 1 - oligo(dT) primer 15',
                TGTATACCAATCTGAAGTGGGAGCGGCGGCGGCAAAATTTTTTTTTTTTTTTT
                T 3', on equal amounts of mRNA from 2 13.5dpc and 2
                14.5dpc embryos [total RNA provided by Minoru Ko, Wayne
                State Univ., from 2 ]; double stranded cDNA was ligated to
                Eco RI adaptors (Pharmacia), digested with Not 1 and
                cloned into the Not 1 and Eco RI sites of the modified
                p773 vector. Library went through one round of
                normalization, and was constructed by Bento Soares and
                M.Fatima Bonaldo."
BASE COUNT     17 a 16 c 19 g 18 t
ORIGIN
Alignment Scores:
Pred. No.:      5,62e+03      Length:      70
Score:          24.00         Matches:      5
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches:      0
Query Match:    100.00%      Indels:       0
DB:             9            Gaps:        0

US 09-856-070-25 (1-5) x AA016604 (1-70)

QY      1 MetLeuArgLeuGln 5
Db      46 ATGCTCAGGCTACAG 22
RESULT  6
AA000474/c

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AA423006/c
LOCUS          AA423006      74 bp      mRNA      linear      EST 16-OCT 1997
DEFINITION     vc84a04.r1 Soares mouse NDMH Mus musculus cDNA clone IMAGE:832878
                5' similar to gb:108441 CYTOCHROME C OXIDASE POLYPEPTIDE III (HUMAN
                );, mRNA sequence.
ACCESSION      AA423006
VERSION        AA423006.1  GI:2101822
KEYWORDS       EST.
SOURCE         house mouse.
ORGANISM       Mus musculus
REFERENCE      Mammalia: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
AUTHORS        Fukuyota; Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Murinae: Mus.
                1 (bases 1 to 74)
                Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
                Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
                Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
                Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                Waterston, R.
TITLE          The WashU-HMI Mouse EST Project
JOURNAL        Unpublished (1996)
COMMENT        Contact: Marra M/Mouse EST Project
                WashU-HMI Mouse EST Project
                Washington University School of Medicine
                4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                Tel: 314 286 1800
                Fax: 314 286 1810
                Email: mouseest@watson.wustl.edu
                This clone is available royalty-free through LLNL ; contact the
                IMAGE Consortium (info@imgc.llnl.gov) for further information.
                MGI:493094
                Trace considered overall poor quality
                Seq primer: -28m13 rev2 ET from Amersham
                High quality sequence stop: 1.
FEATURES       1..74
                Location/Qualifiers
                1..74
                /organism="Mus musculus"
                /strain="C57BL/6J"
                /db_xref="taxon:10090"
                /clone="IMAGE:832878"
                /clone_lib="Soares mouse NDMH"
                /sex="male"
                /tissue_type="heart"
                /dev_stage="4 weeks"
                /lab_host="DH10B"
                /note="Vector: p773D-Pac (Pharmacia) with a modified
                polylinker; Site 1: Not 1; Site 2: Eco RI; 1st strand cDNA
                was primed with a Not 1 - oligo(dT) primer 15',
                TGTATACCAATCTGAAGTGGGAGCGGCGGCGGCAAAATTTTTTTTTTTTTTTT
                T 3'; double stranded cDNA was ligated to Eco RI adaptors
                (Pharmacia), digested with Not 1 and cloned into the Not
                1 and Eco RI sites of the modified p773 vector. RNA
                provided by Dr. Minoru Ko, Wayne State Univ. library
                constructed and normalized by Bento Soares and M.Fatima
                Bonaldo."
BASE COUNT     20 a 17 c 16 g 21 t
ORIGIN
Alignment Scores:
Pred. No.:      5,98e+03      Length:      74
Score:          23.00         Matches:      5
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches:      0
Query Match:    100.00%      Indels:       0
DB:             9            Gaps:        0

US-09-856-070-25 (1-5) x AA423006 (1-74)

QY      1 MetLeuArgLeuGln 5
Db      43 ATGCTCGGCTTCAA 29
RESULT  7
AA600474/c

```


JOURNAL
MEDLINE
COMMENT

Genome Res. 6 (9), 807-828 (1996)
97044478
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est.watson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGe Consortium (infoimage.lnl.gov) for further information.
Seq primer: m3 -40 forward
High quality sequence stop: 1.

FEATURES
source

1..78
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="Gene:1892046"
/db_xref="taxon:9606"
/clone_lib="MAGE:284929"
/issue_type="Cochlea"
/dev_stage="16-22 week fetus"
/lab_host="SOLR cells (Kanamycin resistant)"
/note="Organ: ear; Vector: pBluescript SK+ Site:1: EcoRI;
Site:2: XbaI; Reference: Genomics 23, 42-50 (1994) cloned
unidirectionally. Primer: Oligo dT. Fetal cochlea, normal.
37% of inserts 0.5 kb, 56% 0.5-1.0 kb, 7% >1 kb. Uni-ZAP
XK Vector. Library constructed by N. Robertson, C. Morton
-5' adaptor sequence: 5' GAATTCGGCAGCAG 3' -3' adaptor
sequence: 5' CCGCAGTTTTTTTTTTT 3"

BASE COUNT 14 a 22 c 23 g 19 l
ORIGIN
Alignment Scores:
Pred. No.: 6,46e+03 Length: 78
Score: 24.00 Matches: 5
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US 09 856 070-25 (1-5) x N71860 (1-79)

QY 1 MelLeuArcLeuGln 5
DB 62 ATCTTCAGG-TCGAC 48

RESULT 10
HH218187
LOCUS

HH218187 100607710..Y1 1006 - RescueMu Grid G Zea mays genomic, DNA
sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

HH218187.1 GI:16810650
GSS.
Zea mays.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACG
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 82)

REFERENCE
AUTHORS
JOURNAL
COMMENT

Walbot V.
Maize genomic sequences found using engineered RescueMu Transposon
unpublished (2001)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8223
Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post ligation sequence from source sequence.
Plate: 1006077 row: 27

FEATURES
source

Class: Transposon-tagged.
Location/Qualifiers
1..82
/organism="Zea mays"
/cultural="mixed background W23/A186/H71"
/db_xref="taxon:4577"
/clone_lib="1006 - RescueMu Grid G"
/issue_type="leaf"
/dev_stage="adult"
/lab_host="DH10H"
/note="Organ: leaf, Vector: RescueMu (engineered from
pBluescript backbone); Site:1: BamHI; Site:2: BclII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site 'www.zmdb.tastate.edu' and follow the links for
'RescueMu.' Grid G was grown at Stanford in 2000. DNA was
extracted from leaf punches, double digested using BamHI
and BclII, and ligated to form circular plasmids. DH10B
cells were transformed and then screened on LB plates with
ampicillin."

BASE COUNT 17 a 21 c 20 g 24 t
ORIGIN
Alignment Scores:
Pred. No.: 6,73e+03 Length: 82
Score: 23.00 Matches: 5
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 17 Gaps: 0

US-09-856-070-25 (1-5) x HH218187 (1-82)

QY 1 MelLeuArcLeuGln 5

DB 46 ATG-TGCTCTG-TA; 50
RESULT 11
AA438242/c
LOCUS
DEFINITION
V23303.g1 Knowles Solter mouse 2 cell Mus musculus cDNA clone
IMAGE:743449 5' similar to gp-L08441 CYTOCHROME C OXIDASE
POLYPEPTIDE III (HUMAN);, mRNA sequence.
AA438242
AA438242.1 GI:2143156
EST.
house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 95)
Marra M., Hillier L., Allen M., Bowles M., Dietrich N., Dubuque T.,
Geisler S., Kucaba T., Lacy M., Le M., Martin J., Morris M.,
Schellenberg K., Steptoe M., Tan F., Underwood K., Moore B.,
Thaising B., Wylic L., Lennon G., Soares H., Wilson R. and
Waterston R.
The WashU-HMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGe Consortium (infoimage.lnl.gov) for further information.
MGI:477757
Seq primer: -40m13 fwd. FI from Amersham.
Location/Qualifiers
1..95

FEATURES
source

<p>Site_2: XhoI, Cloned unidirectionally. Primer: oligo dT normal lung. Average insert size: 1.0 kb; SalI ZAP XR Vector; 5' adaptor sequence: 5' GAATTCGACGAG 3' 3' adaptor sequence: 5' CCGCAGTTTTTTTTTTTTT 3'</p> <p>BASE COUNT 18 a 33 c 24 g 23 t</p> <p>ORIGIN</p>	<p>Site_1: MluI, Site_2: SalI, Cloned unidirectionally from mRNA prepared from 13,500 2-cell stage embryos. Primer: SalI(dT): 5'-GCTGATGCTGAGGCTTTTTTTTTT-3' cDNAs were cloned into the MluI/SalI sites of a modified pBluescribe vector using commercial linkers (NEB)</p> <p>Average insert size: 1.2 kb.</p> <p>23 a 20 c 18 g 34 t</p> <p>ORIGIN</p>	<p>Site_2: XhoI, Cloned unidirectionally. Primer: oligo dT normal lung. Average insert size: 1.0 kb; SalI ZAP XR Vector; 5' adaptor sequence: 5' GAATTCGACGAG 3' 3' adaptor sequence: 5' CCGCAGTTTTTTTTTTTTT 3'</p> <p>BASE COUNT 18 a 33 c 24 g 23 t</p> <p>ORIGIN</p>	<p>Site_1: MluI, Site_2: SalI, Cloned unidirectionally from mRNA prepared from 13,500 2-cell stage embryos. Primer: SalI(dT): 5'-GCTGATGCTGAGGCTTTTTTTTTT-3' cDNAs were cloned into the MluI/SalI sites of a modified pBluescribe vector using commercial linkers (NEB)</p> <p>Average insert size: 1.2 kb.</p> <p>23 a 20 c 18 g 34 t</p> <p>ORIGIN</p>
<p>Alignment Scores:</p> <p>Pred. No.: 7.96e+03 Length: 95</p> <p>Score: 21.00 Matches: 5</p> <p>Percent Similarity: 100.00% Conservative: 0</p> <p>Best local Similarity: 100.00% Mismatches: 0</p> <p>Query Match: 100.00% Indels: 0</p> <p>DB: 9 Gaps: 0</p> <p>US-09-856-070-25 (1-5) x AA438242 (1-95)</p>	<p>Alignment Scores:</p> <p>Pred. No.: 7.96e+03 Length: 95</p> <p>Score: 21.00 Matches: 5</p> <p>Percent Similarity: 100.00% Conservative: 0</p> <p>Best local Similarity: 100.00% Mismatches: 0</p> <p>Query Match: 100.00% Indels: 0</p> <p>DB: 9 Gaps: 0</p> <p>US-09-856-070-25 (1-5) x AA438242 (1-95)</p>	<p>Alignment Scores:</p> <p>Pred. No.: 7.96e+03 Length: 98</p> <p>Score: 23.00 Matches: 5</p> <p>Percent Similarity: 100.00% Conservative: 0</p> <p>Best local Similarity: 100.00% Mismatches: 0</p> <p>Query Match: 100.00% Indels: 0</p> <p>DB: 9 Gaps: 0</p> <p>US-09-856-070-25 (1-5) x AA487184 (1-98)</p>	<p>Alignment Scores:</p> <p>Pred. No.: 7.96e+03 Length: 98</p> <p>Score: 23.00 Matches: 5</p> <p>Percent Similarity: 100.00% Conservative: 0</p> <p>Best local Similarity: 100.00% Mismatches: 0</p> <p>Query Match: 100.00% Indels: 0</p> <p>DB: 9 Gaps: 0</p> <p>US-09-856-070-25 (1-5) x AA487184 (1-98)</p>
<p>QY 1 MetLeuArgLeuGln 5</p> <p>Db 28 ATGCTGCGGCTTCAA 14</p> <p>RESULT 12</p> <p>LOCUS AA487184</p> <p>DEFINITION ab013306.sl Stratagene lung (#37210) Homo sapiens cDNA clone IMAGE:841451 3' similar to gb:Z13009_rnal EPITHELIAL-CADHERIN PPECUPSOP (HUMAN); mRNA sequence.</p> <p>ACCESSION AA487184</p> <p>VERSION AA487184.1 GI:2217328</p> <p>KEYWORDS EST.</p> <p>SOURCE human</p> <p>ORGANISM Homo sapiens</p> <p>Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo; 1 (bases 1 to 98)</p> <p>REFERENCE 1 Hillier, L., Allen, M., Howles, L., Dubuque, T., Getzel, G., Jost, S., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, T., Moore, B., Schellenberg, K., Stepien, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R., and Wilson, R</p> <p>WashU-Merck EST Project 1997</p> <p>UNPUBLISHED (1997)</p> <p>CONTACT: Wilson RK</p> <p>Washington University School of Medicine</p> <p>4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108</p> <p>Tel: 314 286 1800</p> <p>Fax: 314 286 1810</p> <p>Email: est@watson.wustl.edu</p> <p>This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.</p> <p>Trace considered overall poor quality</p> <p>Seq primer: -4lm13 fwd. ET from Amersham</p> <p>High quality sequence stop: 1.</p> <p>location/Qualifiers</p> <p>1..98</p> <p>/organism="Homo sapiens"</p> <p>/db_xref="taxon:9606"</p> <p>/clone="IMAGE:841451"</p> <p>/clone.lib="Stratagene lung (#37210)"</p> <p>/sex="male"</p> <p>/dev_stage="72 years"</p> <p>/lab_host="SOLR cells (kanamycin resistant)"</p> <p>/note="organ. lung; Vector: pBluescript SK-; Site 1: EcoRI</p>	<p>QY 1 MetLeuArgLeuGln 5</p> <p>Db 28 ATGCTGCGGCTTCAA 14</p> <p>RESULT 12</p> <p>LOCUS AA487184</p> <p>DEFINITION ab013306.sl Stratagene lung (#37210) Homo sapiens cDNA clone IMAGE:841451 3' similar to gb:Z13009_rnal EPITHELIAL-CADHERIN PPECUPSOP (HUMAN); mRNA sequence.</p> <p>ACCESSION AA487184</p> <p>VERSION AA487184.1 GI:2217328</p> <p>KEYWORDS EST.</p> <p>SOURCE human</p> <p>ORGANISM Homo sapiens</p> <p>Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo; 1 (bases 1 to 98)</p> <p>REFERENCE 1 Hillier, L., Allen, M., Howles, L., Dubuque, T., Getzel, G., Jost, S., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, T., Moore, B., Schellenberg, K., Stepien, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R., and Wilson, R</p> <p>WashU-Merck EST Project 1997</p> <p>UNPUBLISHED (1997)</p> <p>CONTACT: Wilson RK</p> <p>Washington University School of Medicine</p> <p>4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108</p> <p>Tel: 314 286 1800</p> <p>Fax: 314 286 1810</p> <p>Email: est@watson.wustl.edu</p> <p>This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.</p> <p>Trace considered overall poor quality</p> <p>Seq primer: -4lm13 fwd. ET from Amersham</p> <p>High quality sequence stop: 1.</p> <p>location/Qualifiers</p> <p>1..98</p> <p>/organism="Homo sapiens"</p> <p>/db_xref="taxon:9606"</p> <p>/clone="IMAGE:841451"</p> <p>/clone.lib="Stratagene lung (#37210)"</p> <p>/sex="male"</p> <p>/dev_stage="72 years"</p> <p>/lab_host="SOLR cells (kanamycin resistant)"</p> <p>/note="organ. lung; Vector: pBluescript SK-; Site 1: EcoRI</p>	<p>QY 1 MetLeuArgLeuGln 5</p> <p>Db 75 ATGCTGCGATTACAG 89</p> <p>RESULT 13</p> <p>LOCUS HF448833</p> <p>DEFINITION nae33h10.x1 Lupski, sympathetic trunk Homo sapiens cDNA clone IMAGE:4090986 3', mRNA sequence.</p> <p>ACCESSION HF448833</p> <p>VERSION HF448833.1 GI:11515002</p> <p>KEYWORDS EST.</p> <p>SOURCE human.</p> <p>ORGANISM Homo sapiens</p> <p>Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo; 1 (bases 1 to 99)</p> <p>REFERENCE 1 National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index</p> <p>UNPUBLISHED (1997)</p> <p>CONTACT: Robert Strausberg, Ph.D.</p> <p>Email: cgapbs@mail.nih.gov</p> <p>Tissue procurement: Dr. James Lupski</p> <p>cDNA Library Preparation: Lupski Laboratory</p> <p>cDNA Library Arrayed by: The I M A G E Consortium (LLNL)</p> <p>DNA Sequencing by: Washington University Genome Sequencing Center</p> <p>Clone distribution: NCI-CGAP clone distribution information can be found through the I M A G E Consortium/LLNL at: info@image.llnl.gov</p> <p>Seq primer: -40VP from Gibco</p> <p>High quality sequence stop: 87.</p> <p>location/Qualifiers</p> <p>1..99</p> <p>/organism="Homo sapiens"</p> <p>/db_xref="taxon:9606"</p> <p>/clone="IMAGE:4090986"</p> <p>/clone.lib="Lupski_sympathetic_trunk"</p> <p>/sex="male"</p> <p>/tissue_type="sympathetic trunk"</p> <p>/dev_stage="adult, 16 yr"</p> <p>/lab_host="DH10B"</p> <p>/note="Vector: pCMV-SPORT6 (Life Technologies); Site 1: NotI; Site 2: SalI; cDNA made by oligo-dT priming.</p> <p>Directionally cloned using the following adaptors:</p> <p>5'-GCTAGTCTTCAAGTCGCGAGGGGGGGGGG(15)-3' Size selected > 1 kb for average insert length 1.9 kb. This is a primary library, non-amplified library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine); available through Life Technologies."</p> <p>36 a 15 c 18 g 30 t</p> <p>BASE COUNT</p> <p>ORIGIN</p> <p>Alignment Scores:</p>	<p>QY 1 MetLeuArgLeuGln 5</p> <p>Db 75 ATGCTGCGATTACAG 89</p> <p>RESULT 13</p> <p>LOCUS HF448833</p> <p>DEFINITION nae33h10.x1 Lupski, sympathetic trunk Homo sapiens cDNA clone IMAGE:4090986 3', mRNA sequence.</p> <p>ACCESSION HF448833</p> <p>VERSION HF448833.1 GI:11515002</p> <p>KEYWORDS EST.</p> <p>SOURCE human.</p> <p>ORGANISM Homo sapiens</p> <p>Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo; 1 (bases 1 to 99)</p> <p>REFERENCE 1 National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index</p> <p>UNPUBLISHED (1997)</p> <p>CONTACT: Robert Strausberg, Ph.D.</p> <p>Email: cgapbs@mail.nih.gov</p> <p>Tissue procurement: Dr. James Lupski</p> <p>cDNA Library Preparation: Lupski Laboratory</p> <p>cDNA Library Arrayed by: The I M A G E Consortium (LLNL)</p> <p>DNA Sequencing by: Washington University Genome Sequencing Center</p> <p>Clone distribution: NCI-CGAP clone distribution information can be found through the I M A G E Consortium/LLNL at: info@image.llnl.gov</p> <p>Seq primer: -40VP from Gibco</p> <p>High quality sequence stop: 87.</p> <p>location/Qualifiers</p> <p>1..99</p> <p>/organism="Homo sapiens"</p> <p>/db_xref="taxon:9606"</p> <p>/</p>

Pred. No.: 8.93e+03 Length: 105
 Score: 23.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 10 Gaps: 0

US-09-856-070-25 (1-5) x AW863056 (1-105)

QY 1 MetLeuArgLeuGln 5

DB 37 ATGCTAGACTTCAG 51

Search completed: January 16, 2003, 21:37:11
 Job time : 665.571 secs

